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SEQUENCE LISTING

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<120> SERINE PROTEINASE INHIBITORS

<130> 10496/P65678US0

<140> 09/582,328

<141> 2000-07-19

<150> PCT/EP98/08424

<151> 1998-12-23

<150> DE 197 57 572.2

<151> 1997-12-23

<160> 41

<170> PatentIn Ver. 2.1

<210> 1

<211> 177

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: VAKTI-1 amino
acid sequence

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Met Lys Ile Ala Thr Val Ser Val Leu Leu Pro Leu Ala Leu Cys Leu
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Ile Gln Asp Ala Ala Ser Lys Asn Glu Asp Gln Glu Met Cys His Glu
20 25 30

Phe Gln Ala Phe Met Lys Asn Gly Lys Leu Phe Cys Pro Gln Asp Lys
35 40 45

Lys Phe Phe Gln Ser Leu Asp Gly Ile Met Phe Ile Asn Lys Cys Ala
50 55 60

Thr Cys Lys Met Ile Leu Glu Lys Glu Ala Lys Ser Gln Lys Arg Ala
65 70 75 80

Arg His Leu Ala Arg Ala Pro Lys Ala Thr Ala Pro Thr Glu Leu Asn
85 90 95

Cys Asp Asp Phe Lys Lys Gly Glu Arg Asp Gly Asp Phe Ile Cys Pro
100 105 110

Asp Tyr Tyr Glu Ala Val Cys Gly Thr Asp Gly Lys Thr Tyr Asp Asn
115 120 125

Arg Cys Ala Leu Cys Ala Glu Asn Ala Lys Thr Gly Ser Gln Ile Gly
 130 135 140

Val Lys Ser Glu Gly Glu Cys Lys Ser Ser Asn Pro Glu Gln Val Arg
 145 150 155 160

Ser Ile Val Ser Leu Met Gly Asn Thr Gly Arg Leu Thr Ser Asn Ser
 165 170 175

Lys

<210> 2

<211> 922

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: VATKI-2 amino
 acid sequence

<400> 2

Met Lys Ile Ala Thr Val Ser Val Leu Leu Pro Leu Ala Leu Cys Leu
 1 5 10 15

Ile Gln Asp Ala Ala Ser Lys Asn Glu Asp Gln Glu Met Cys His Glu
 20 25 30

Phe Gln Ala Phe Met Lys Asn Gly Lys Leu Phe Cys Pro Gln Asp Lys
 35 40 45

Lys Phe Phe Gln Ser Leu Asp Gly Ile Met Phe Ile Asn Lys Cys Ala
 50 55 60

Thr Cys Lys Met Ile Leu Glu Lys Glu Ala Lys Ser Gln Lys Arg Ala
 65 70 75 80

Arg His Leu Ala Arg Ala Pro Lys Ala Thr Ala Pro Thr Glu Leu Asn
 85 90 95

Cys Asp Asp Phe Lys Lys Gly Glu Arg Asp Gly Asp Phe Ile Cys Pro
 100 105 110

Asp Tyr Tyr Glu Ala Val Cys Gly Thr Asp Gly Lys Thr Tyr Asp Asn
 115 120 125

Arg Cys Ala Leu Cys Ala Glu Asn Ala Lys Thr Gly Ser Gln Ile Gly
 130 135 140

Val Lys Ser Glu Gly Glu Cys Lys Ser Ser Asn Pro Glu Gln Asp Val
 145 150 155 160

Cys Ser Ala Phe Arg Pro Phe Val Arg Asn Gly Arg Leu Gly Cys Thr
 165 170 175

Arg Glu Asn Asp Pro Val Leu Gly Pro Asp Gly Lys Thr His Gly Asn
 180 185 190

Lys Cys Ala Met Cys Ala Glu Leu Phe Leu Lys Glu Ala Glu Asn Ala
 195 200 205
 Lys Arg Glu Gly Glu Thr Arg Ile Arg Arg Asn Ala Glu Lys Asp Phe
 210 215 220
 Cys Lys Glu Tyr Glu Lys Gln Val Arg Asn Gly Arg Leu Phe Cys Thr
 225 230 235 240
 Arg Glu Ser Asp Pro Val Arg Gly Pro Asp Gly Arg Met His Gly Asn
 245 250 255
 Lys Cys Ala Leu Cys Ala Glu Ile Phe Lys Arg Arg Phe Ser Glu Glu
 260 265 270
 Asn Ser Lys Thr Asp Gln Asn Leu Gly Lys Ala Glu Glu Lys Thr Lys
 275 280 285
 Val Lys Arg Glu Ile Val Lys Leu Cys Ser Gln Tyr Gln Asn Gln Ala
 290 295 300
 Lys Asn Gly Ile Leu Phe Cys Thr Arg Glu Asn Asp Pro Ile Arg Gly
 305 310 315 320
 Pro Asp Gly Lys Met His Gly Asn Leu Cys Ser Met Cys Gln Val Tyr
 325 330 335
 Phe Gln Ala Glu Asn Glu Glu Lys Lys Lys Ala Glu Ala Arg Ala Arg
 340 345 350
 Asn Lys Arg Glu Ser Gly Lys Ala Thr Ser Tyr Ala Glu Leu Cys Asn
 355 360 365
 Glu Tyr Arg Lys Leu Val Arg Asn Gly Lys Leu Ala Cys Thr Arg Glu
 370 375 380
 Asn Asp Pro Ile Gln Gly Pro Asp Gly Lys Val His Gly Asn Thr Cys
 385 390 395 400
 Ser Met Cys Glu Val Phe Phe Gln Ala Glu Glu Glu Glu Lys Lys Lys
 405 410 415
 Lys Glu Gly Glu Ser Arg Asn Lys Arg Gln Ser Lys Ser Thr Ala Ser
 420 425 430
 Phe Glu Glu Leu Cys Ser Glu Tyr Arg Lys Ser Arg Lys Asn Gly Arg
 435 440 445
 Leu Phe Cys Thr Arg Glu Asn Asp Pro Ile Gln Gly Pro Asp Gly Lys
 450 455 460
 Met His Gly Asn Thr Cys Ser Met Cys Glu Ala Phe Phe Gln Gln Glu
 465 470 475 480
 Glu Arg Ala Arg Ala Lys Ala Lys Arg Glu Ala Ala Lys Glu Ile Cys
 485 490 495

Ser Glu Phe Arg Asp Gln Val Arg Asn Gly Thr Leu Ile Cys Thr Arg
 500 505 510
 Glu His Asn Pro Val Arg Gly Pro Asp Gly Lys Met His Gly Asn Lys
 515 520 525
 Cys Ala Met Cys Ala Ser Val Phe Lys Leu Glu Glu Glu Glu Lys Lys
 530 535 540
 Asn Asp Lys Glu Glu Lys Gly Lys Val Glu Ala Glu Lys Val Lys Arg
 545 550 555 560
 Glu Ala Val Gln Glu Leu Cys Ser Glu Tyr Arg His Tyr Val Arg Asn
 565 570 575
 Gly Arg Leu Pro Cys Thr Arg Glu Asn Asp Pro Ile Glu Gly Leu Asp
 580 585 590
 Gly Lys Ile His Gly Asn Thr Cys Ser Met Cys Glu Ala Phe Phe Gln
 595 600 605
 Gln Glu Ala Lys Glu Lys Glu Arg Ala Glu Pro Arg Ala Lys Val Lys
 610 615 620
 Arg Glu Ala Glu Lys Glu Thr Cys Asp Glu Phe Arg Arg Leu Leu Gln
 625 630 635 640
 Asn Gly Lys Leu Phe Cys Thr Arg Glu Asn Asp Pro Val Arg Gly Pro
 645 650 655
 Asp Gly Lys Thr His Gly Asn Lys Cys Ala Met Cys Lys Ala Val Phe
 660 665 670
 Gln Lys Glu Asn Glu Glu Arg Lys Arg Lys Glu Glu Glu Asp Gln Arg
 675 680 685
 Asn Ala Ala Gly His Gly Ser Ser Gly Gly Gly Gly Gly Asn Thr Gln
 690 695 700
 Asp Glu Cys Ala Glu Tyr Arg Glu Gln Met Lys Asn Gly Arg Leu Ser
 705 710 715 720
 Cys Thr Arg Glu Ser Asp Pro Val Arg Asp Ala Asp Gly Lys Ser Tyr
 725 730 735
 Asn Asn Gln Cys Thr Met Cys Lys Ala Lys Leu Glu Arg Glu Ala Glu
 740 745 750
 Arg Lys Asn Glu Tyr Ser Arg Ser Arg Ser Asn Gly Thr Gly Ser Glu
 755 760 765
 Ser Gly Lys Asp Thr Cys Asp Glu Phe Arg Ser Gln Met Lys Asn Gly
 770 775 780
 Lys Leu Ile Cys Thr Arg Glu Ser Asp Pro Val Arg Gly Pro Asp Gly
 785 790 795 800

Lys Thr His Gly Asn Lys Cys Thr Met Cys Lys Glu Lys Leu Glu Arg
 805 810 815

Glu Ala Ala Glu Lys Lys Arg Lys Arg Met Lys Thr Gly Ala Ile Gln
 820 825 830

Glu Lys Gly Ala Ile Gln Glu Lys Gly Ala Met Thr Lys Arg Ile Cys
 835 840 845

Val Val Asn Phe Glu Ala Cys Arg Glu Met Glu Ser Leu Ser Ala Pro
 850 855 860

Glu Lys Ile Thr Leu Phe Glu Ala His Met Ala Arg Cys Thr Ser Ile
 865 870 875 880

Asn Val Leu Cys Val Arg Ala Ser Leu Ile Glu Lys Leu Met Lys Glu
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Lys Arg Lys Met Lys Arg Asn Gln Val Ala Ser Pro Gln Ile Met Gln
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Arg Met Ser Ala Val Asn Phe Glu Thr Ile
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<210> 3

<211> 55

<212> PRT

<213> Unknown Organism

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<223> Description of Unknown Organism: HF 6479 amino
 acid sequence

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Asp Gly Ile Met Phe Ile Asn Lys Cys Ala Thr Cys Lys Met Ile Leu
 35 40 45

Glu Lys Glu Ala Lys Ser Gln
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<210> 4

<211> 68

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: HF 7665 amino
 acid sequence

<400> 4

Glu Ser Gly Lys Ala Thr Ser Tyr Ala Glu Leu Cys Asn Glu Tyr Arg
 1 5 10 15

Lys Leu Val Arg Asn Gly Lys Leu Ala Cys Thr Arg Glu Asn Asp Pro
 20 25 30

Ile Gln Gly Pro Asp Gly Lys Val His Gly Asn Thr Cys Ser Met Cys
 35 40 45

Glu Val Phe Phe Gln Ala Glu Glu Glu Glu Lys Lys Lys Lys Glu Gly
 50 55 60

Glu Ser Arg Asn
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<210> 5

<211> 748

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: VAKTI-1 cDNA
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<220>

<221> CDS

<222> (43)..(573)

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 Thr Val Ser Val Leu Leu Pro Leu Ala Leu Cys Leu Ile Gln Asp Ala
 5 10 15 20

gcc agt aag aat gaa gat cag gaa atg tgc cat gaa ttt cag gca ttt 150
 Ala Ser Lys Asn Glu Asp Gln Glu Met Cys His Glu Phe Gln Ala Phe
 25 30 35

atg aaa aat gga aaa ctg ttc tgt ccc cag gat aag aaa ttt ttt caa 198
 Met Lys Asn Gly Lys Leu Phe Cys Pro Gln Asp Lys Lys Phe Phe Gln
 40 45 50

agt ctt gat gga ata atg ttc atc aat aaa tgt gcc acg tgc aaa atg 246
 Ser Leu Asp Gly Ile Met Phe Ile Asn Lys Cys Ala Thr Cys Lys Met
 55 60 65

ata ctg gaa aaa gaa gca aaa tca cag aag agg gcc agg cat tta gca 294
 Ile Leu Glu Lys Glu Ala Lys Ser Gln Lys Arg Ala Arg His Leu Ala
 70 75 80

aga gct ccc aag gct act gcc cca aca gag ctg aat tgt gat gat ttt 342
 Arg Ala Pro Lys Ala Thr Ala Pro Thr Glu Leu Asn Cys Asp Asp Phe
 85 90 95 100

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aaa aaa gga gaa aga gat ggg gat ttt atc tgt cct gat tat tat gaa 390
Lys Lys Gly Glu Arg Asp Gly Asp Phe Ile Cys Pro Asp Tyr Tyr Glu
      105                      110                      115

gct gtt tgt ggc aca gat ggg aaa aca tat gac aac aga tgt gca ctg 438
Ala Val Cys Gly Thr Asp Gly Lys Thr Tyr Asp Asn Arg Cys Ala Leu
      120                      125                      130

tgt gct gag aat gcg aaa acc ggg tcc caa att ggt gta aaa agt gaa 486
Cys Ala Glu Asn Ala Lys Thr Gly Ser Gln Ile Gly Val Lys Ser Glu
      135                      140                      145

ggg gaa tgt aag agc agt aat cca gag cag gtg agg tca att gtc agc 534
Gly Glu Cys Lys Ser Ser Asn Pro Glu Gln Val Arg Ser Ile Val Ser
      150                      155                      160

ctg atg gga aat act ggg agg cta act tca aat agt aag taggtgctgt 583
Leu Met Gly Asn Thr Gly Arg Leu Thr Ser Asn Ser Lys
      165                      170                      175

cctcttcctt cttaggtggg agccttgga ggaattaatt cttgctttat gtgaaatgga 643

ataccaggtt actgcccact aatatgaaaa agctaattat agtctctgaa actggatcag 703

attactttgg tggttaagat ctttcaatct attgctgctt tgtat 748

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 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: VATKI-2 cDNA
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<220>
 <221> CDS
 <222> (43)..(2808)

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Thr Val Ser Val Leu Leu Pro Leu Ala Leu Cys Leu Ile Gln Asp Ala
      5                      10                      15                      20

gcc agt aag aat gaa gat cag gaa atg tgc cat gaa ttt cag gca ttt 150
Ala Ser Lys Asn Glu Asp Gln Glu Met Cys His Glu Phe Gln Ala Phe
      25                      30                      35

atg aaa aat gga aaa ctg ttc tgt ccc cag gat aag aaa ttt ttt caa 198
Met Lys Asn Gly Lys Leu Phe Cys Pro Gln Asp Lys Lys Phe Phe Gln
      40                      45                      50

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agt ctt gat gga ata atg ttc atc aat aaa tgt gcc acg tgc aaa atg 246
 Ser Leu Asp Gly Ile Met Phe Ile Asn Lys Cys Ala Thr Cys Lys Met
 55 60 65

ata ctg gaa aaa gaa gca aaa tca cag aag agg gcc agg cat tta gca 294
 Ile Leu Glu Lys Glu Ala Lys Ser Gln Lys Arg Ala Arg His Leu Ala
 70 75 80

aga gct ccc aag gct act gcc cca aca gag ctg aat tgt gat gat ttt 342
 Arg Ala Pro Lys Ala Thr Ala Pro Thr Glu Leu Asn Cys Asp Asp Phe
 85 90 95 100

aaa aaa gga gaa aga gat ggg gat ttt atc tgt cct gat tat tat gaa 390
 Lys Lys Gly Glu Arg Asp Gly Asp Phe Ile Cys Pro Asp Tyr Tyr Glu
 105 110 115

gct gtt tgt ggc aca gat ggg aaa aca tat gac aac aga tgt gca ctg 438
 Ala Val Cys Gly Thr Asp Gly Lys Thr Tyr Asp Asn Arg Cys Ala Leu
 120 125 130

tgt gct gag aat gcg aaa acc ggg tcc caa att ggt gta aaa agt gaa 486
 Cys Ala Glu Asn Ala Lys Thr Gly Ser Gln Ile Gly Val Lys Ser Glu
 135 140 145

ggg gaa tgt aag agc agt aat cca gag cag gat gta tgc agt gct ttt 534
 Gly Glu Cys Lys Ser Ser Asn Pro Glu Gln Asp Val Cys Ser Ala Phe
 150 155 160

61
 cct
 cgg ccc ttt gtt aga aat gga aga ctt gga tgc aca agg gaa aat gat 582
 Arg Pro Phe Val Arg Asn Gly Arg Leu Gly Cys Thr Arg Glu Asn Asp
 165 170 175 180

cct gtt ctt ggt cct gat ggg aag acg cat ggc aat aag tgt gca atg 630
 Pro Val Leu Gly Pro Asp Gly Lys Thr His Gly Asn Lys Cys Ala Met
 185 190 195

tgt gct gag ctg ttt tta aaa gaa gct gaa aat gcc aag cga gag ggt 678
 Cys Ala Glu Leu Phe Leu Lys Glu Ala Glu Asn Ala Lys Arg Glu Gly
 200 205 210

gaa act aga att cga cga aat gct gaa aag gat ttt tgc aag gaa tat 726
 Glu Thr Arg Ile Arg Arg Asn Ala Glu Lys Asp Phe Cys Lys Glu Tyr
 215 220 225

gaa aaa caa gtg aga aat gga agg ctt ttt tgt aca cgg gag agt gat 774
 Glu Lys Gln Val Arg Asn Gly Arg Leu Phe Cys Thr Arg Glu Ser Asp
 230 235 240

cca gtc cgt ggc cct gac ggc agg atg cat ggc aac aaa tgt gcc ctg 822
 Pro Val Arg Gly Pro Asp Gly Arg Met His Gly Asn Lys Cys Ala Leu
 245 250 255 260

tgt gct gaa att ttc aag cgg cgt ttt tca gag gaa aac agt aaa aca 870
 Cys Ala Glu Ile Phe Lys Arg Arg Phe Ser Glu Glu Asn Ser Lys Thr
 265 270 275

gat caa aat ttg gga aaa gct gaa gaa aaa act aaa gtt aaa aga gaa	918
Asp Gln Asn Leu Gly Lys Ala Glu Glu Lys Thr Lys Val Lys Arg Glu	
280 285 290	
att gtg aaa ctc tgc agt caa tat caa aat cag gca aag aat gga ata	966
Ile Val Lys Leu Cys Ser Gln Tyr Gln Asn Gln Ala Lys Asn Gly Ile	
295 300 305	
ctt ttc tgt acc aga gaa aat gac cct att cgt ggt cca gat ggg aaa	1014
Leu Phe Cys Thr Arg Glu Asn Asp Pro Ile Arg Gly Pro Asp Gly Lys	
310 315 320	
atg cat ggc aac ttg tgt tcc atg tgt caa gtc tac ttc caa gca gaa	1062
Met His Gly Asn Leu Cys Ser Met Cys Gln Val Tyr Phe Gln Ala Glu	
325 330 335 340	
aat gaa gaa aag aaa aag gct gaa gca cga gct aga aac aaa aga gaa	1110
Asn Glu Glu Lys Lys Lys Ala Glu Ala Arg Ala Arg Asn Lys Arg Glu	
345 350 355	
tct gga aaa gca acc tca tat gca gag ctt tgc aat gaa tat cga aag	1158
Ser Gly Lys Ala Thr Ser Tyr Ala Glu Leu Cys Asn Glu Tyr Arg Lys	
360 365 370	
ctt gtg agg aac gga aaa ctt gct tgc acc aga gag aac gat cct att	1206
Leu Val Arg Asn Gly Lys Leu Ala Cys Thr Arg Glu Asn Asp Pro Ile	
375 380 385	
cag ggc cca gat ggg aaa gtg cac ggc aac acc tgc tcc atg tgt gag	1254
Gln Gly Pro Asp Gly Lys Val His Gly Asn Thr Cys Ser Met Cys Glu	
390 395 400	
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Val Phe Phe Gln Ala Glu Glu Glu Glu Lys Lys Lys Lys Glu Gly Glu	
405 410 415 420	
tca aga aac aaa aga caa tct aag agt aca gct tcc ttt gag gag ttg	1350
Ser Arg Asn Lys Arg Gln Ser Lys Ser Thr Ala Ser Phe Glu Glu Leu	
425 430 435	
tgt agt gaa tac cgc aaa tcc agg aaa aac gga cgg ctt ttt tgc acc	1398
Cys Ser Glu Tyr Arg Lys Ser Arg Lys Asn Gly Arg Leu Phe Cys Thr	
440 445 450	
aga gag aat gac ccc atc cag ggc cca gat ggg aaa atg cat ggc aac	1446
Arg Glu Asn Asp Pro Ile Gln Gly Pro Asp Gly Lys Met His Gly Asn	
455 460 465	
acc tgc tcc atg tgt gag gcc ttc ttt caa caa gaa gaa aga gca aga	1494
Thr Cys Ser Met Cys Glu Ala Phe Phe Gln Gln Glu Glu Arg Ala Arg	
470 475 480	
gca aag gct aaa aga gaa gct gca aag gaa atc tgc agt gaa ttt cgg	1542
Ala Lys Ala Lys Arg Glu Ala Ala Lys Glu Ile Cys Ser Glu Phe Arg	
485 490 495 500	

gac caa gtg agg aat gga aca ctt ata tgc acc agg gag cat aat cct	1590
Asp Gln Val Arg Asn Gly Thr Leu Ile Cys Thr Arg Glu His Asn Pro	
505 510 515	
gtc cgt gga cca gat ggc aaa atg cat gga aac aag tgt gcc atg tgt	1638
Val Arg Gly Pro Asp Gly Lys Met His Gly Asn Lys Cys Ala Met Cys	
520 525 530	
gcc agt gtg ttc aaa ctt gaa gaa gaa gag aag aaa aat gat aaa gaa	1686
Ala Ser Val Phe Lys Leu Glu Glu Glu Lys Lys Asn Asp Lys Glu	
535 540 545	
gaa aaa ggg aaa gtt gag gct gaa aaa gtt aag aga gaa gca gtt cag	1734
Glu Lys Gly Lys Val Glu Ala Glu Lys Val Lys Arg Glu Ala Val Gln	
550 555 560	
gag ctg tgc agt gaa tat cgt cat tat gtg agg aat gga cga ctc ccc	1782
Glu Leu Cys Ser Glu Tyr Arg His Tyr Val Arg Asn Gly Arg Leu Pro	
565 570 575 580	
tgt acc aga gag aat gat cct att gag ggt cta gat ggg aaa atc cac	1830
Cys Thr Arg Glu Asn Asp Pro Ile Glu Gly Leu Asp Gly Lys Ile His	
585 590 595	
ggc aac acc tgc tcc atg tgt gaa gcc ttc ttc cag caa gaa gca aaa	1878
Gly Asn Thr Cys Ser Met Cys Glu Ala Phe Phe Gln Gln Glu Ala Lys	
600 605 610	
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Glu Lys Glu Arg Ala Glu Pro Arg Ala Lys Val Lys Arg Glu Ala Glu	
615 620 625	
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Lys Glu Thr Cys Asp Glu Phe Arg Arg Leu Leu Gln Asn Gly Lys Leu	
630 635 640	
ttc tgc aca aga gaa aat gat cct gtg cgt ggc cca gat ggc aag acc	2022
Phe Cys Thr Arg Glu Asn Asp Pro Val Arg Gly Pro Asp Gly Lys Thr	
645 650 655 660	
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His Gly Asn Lys Cys Ala Met Cys Lys Ala Val Phe Gln Lys Glu Asn	
665 670 675	
gag gaa aga aag agg aaa gaa gag gaa gat cag aga aat gct gca gga	2118
Glu Glu Arg Lys Arg Lys Glu Glu Glu Asp Gln Arg Asn Ala Ala Gly	
680 685 690	
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His Gly Ser Ser Gly Gly Gly Gly Asn Thr Gln Asp Glu Cys Ala	
695 700 705	
gag tat cgg gaa caa atg aaa aat gga aga ctc agc tgt act cgg gag	2214
Glu Tyr Arg Glu Gln Met Lys Asn Gly Arg Leu Ser Cys Thr Arg Glu	
710 715 720	

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 Ser Asp Pro Val Arg Asp Ala Asp Gly Lys Ser Tyr Asn Asn Gln Cys
 725 730 735 740

acc atg tgt aaa gca aaa ttg gaa aga gaa gca gag aga aaa aat gag 2310
 Thr Met Cys Lys Ala Lys Leu Glu Arg Glu Ala Glu Arg Lys Asn Glu
 745 750 755

tat tct cgc tcc aga tca aat ggg act gga tca gaa tca ggg aag gat 2358
 Tyr Ser Arg Ser Arg Ser Asn Gly Thr Gly Ser Glu Ser Gly Lys Asp
 760 765 770

aca tgt gat gag ttt aga agc caa atg aaa aat gga aaa ctt atc tgc 2406
 Thr Cys Asp Glu Phe Arg Ser Gln Met Lys Asn Gly Lys Leu Ile Cys
 775 780 785

act cga gaa agt gac cct gtc cgg ggt cca gat ggc aag aca cat ggt 2454
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 790 795 800

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 Asn Lys Cys Thr Met Cys Lys Glu Lys Leu Glu Arg Glu Ala Ala Glu
 805 810 815 820

aaa aaa aga aag agg atg aag aca gga gca ata cag gag aaa gga gca 2550
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 825 830 835

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 855 860 865

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 870 875 880

gtc aga gca tct ttg atc gag aag cta atg aaa gaa aaa aga aag atg 2742
 Val Arg Ala Ser Leu Ile Glu Lys Leu Met Lys Glu Lys Arg Lys Met
 885 890 895 900

aag aga aat caa gta gca agc cct caa ata atg caa agg atg agt gca 2790
 Lys Arg Asn Gln Val Ala Ser Pro Gln Ile Met Gln Arg Met Ser Ala
 905 910 915

gtg aat ttc gaa act ata taaggaacaa tgaactcatc tgccctagag 2838
 Val Asn Phe Glu Thr Ile
 920

agaatgaccc agtgcacggt gctgatggaa agttctatac aaacaagtgc tacatgtgca 2898

gagctgtctt tctaacagaa gctttggaaa gggcaaagct tcaagaaaaa ccatcccatg 2958

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<210> 7
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 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Serine protease
 inhibitor

<400> 7
 His Glu Phe Gln Ala Phe Met Lys Asn Gly Lys Leu Phe
 1 5 10

<210> 8
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 inhibitor

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 1 5 10

<210> 9
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 inhibitor

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<223> Description of Unknown Organism: Serine protease inhibitor

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<223> Description of Unknown Organism: Serine protease inhibitor

<400> 11

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<223> Description of Unknown Organism: Serine protease inhibitor

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<223> Description of Unknown Organism: Serine protease inhibitor

<400> 13

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<210> 14

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<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Serine protease
 inhibitor

<400> 14

Asp Glu Phe Arg Arg Leu Leu Gln Asn Gly Lys Leu Phe
 1 5 10

<210> 15

<211> 13

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Serine protease
 inhibitor

<400> 15

Ser Gln Tyr Gln Asn Gln Ala Lys Asn Gly Ile Leu Phe
 1 5 10

<210> 16

<211> 13

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Serine protease
 inhibitor

<400> 16

Ala Glu Tyr Arg Glu Gln Met Lys Asn Gly Arg Leu Ser
 1 5 10

<210> 17

<211> 13

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Serine protease
 inhibitor

<400> 17

Asn Glu Tyr Arg Lys Leu Val Arg Asn Gly Lys Leu Ala
 1 5 10

<210> 18

<211> 13

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Serine protease
 inhibitor

<400> 18

Asp Glu Phe Arg Ser Gln Met Lys Asn Gly Lys Leu Ile
 1 5 10

<210> 19

<211> 18

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Serine protease
 inhibitor

<400> 19

Pro Gln Asp Lys Lys Phe Phe Gln Ser Leu Asp Gly Ile Met Phe Ile
 1 5 10 15

b
int.
 Asn Lys

<210> 20

<211> 18

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Serine protease
 inhibitor

<400> 20

Thr Arg Glu Asn Asp Pro Ile Gln Gly Pro Asp Gly Lys Met His Gly
 1 5 10 15

Asn Thr

<210> 21

<211> 18

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Serine protease
inhibitor

<400> 21

Thr	Arg	Glu	Asn	Asp	Pro	Val	Leu	Gly	Pro	Asp	Gly	Lys	Thr	His	Gly
1				5					10					15	

Asn Lys

<210> 22

<211> 18

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Serine protease
inhibitor

<400> 22

Thr	Arg	Glu	His	Asn	Pro	Val	Arg	Gly	Pro	Asp	Gly	Lys	Met	His	Gly
1				5					10					15	

Asn Lys

<210> 23

<211> 18

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Serine protease
inhibitor

<400> 23

Thr	Arg	Glu	Ser	Asp	Pro	Val	Arg	Gly	Pro	Asp	Gly	Arg	Met	His	Gly
1				5					10					15	

Asn Lys

<210> 24

<211> 18

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Serine protease
inhibitor

<400> 24

Thr Arg Glu Asn Asp Pro Ile Glu Gly Leu Asp Gly Lys Ile His Gly
 1 5 10 15

Asn Thr

<210> 25

<211> 18

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Serine protease
 inhibitor

<400> 25

Thr Arg Glu Asn Asp Pro Ile Arg Gly Pro Asp Gly Lys Met His Gly
 1 5 10 15

Asn Leu

<210> 26

<211> 18

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Serine protease
 inhibitor

<400> 26

Thr Arg Glu Asn Asp Pro Val Arg Gly Pro Asp Gly Lys Thr His Gly
 1 5 10 15

Asn Lys

<210> 27

<211> 18

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Serine protease
 inhibitor

<400> 27

Thr Arg Glu Asn Asp Pro Ile Gln Gly Pro Asp Gly Lys Val His Gly
 1 5 10 15

Asn Thr

<210> 28
 <211> 18
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Serine protease
 inhibitor

<400> 28
 Thr Arg Glu Ser Asp Pro Val Arg Asp Ala Asp Gly Lys Ser Tyr Asn
 1 5 10 15

Asn Gln

<210> 29
 <211> 18
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Serine protease
 inhibitor

<400> 29
 Thr Arg Glu Ser Asp Pro Val Arg Gly Pro Asp Gly Lys Thr His Gly
 1 5 10 15

Asn Lys

<210> 30
 <211> 37
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Serine protease
 inhibitor

<400> 30
 Cys His Glu Phe Gln Ala Phe Met Lys Asn Gly Lys Leu Phe Cys Pro
 1 5 10 15

Gln Asp Lys Lys Phe Phe Gln Ser Leu Asp Gly Ile Met Phe Ile Asn
 20 25 30

Lys Cys Ala Thr Cys
 35

<210> 31
 <211> 37

<212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Serine protease
 inhibitor

<400> 31
 Cys Asp Asp Phe Lys Lys Gly Glu Arg Asp Gly Asp Phe Ile Cys Pro
 1 5 10 15
 Asp Tyr Tyr Glu Ala Val Cys Gly Thr Asp Gly Lys Thr Tyr Asp Asn
 20 25 30
 Arg Cys Ala Leu Cys
 35

<210> 32
 <211> 37
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Serine protease
 inhibitor

<400> 32
 Cys Ser Ala Phe Arg Pro Phe Val Arg Asn Gly Arg Leu Gly Cys Thr
 1 5 10 15
 Arg Glu Asn Asp Pro Val Leu Gly Pro Asp Gly Lys Thr His Gly Asn
 20 25 30
 Lys Cys Ala Met Cys
 35

<210> 33
 <211> 37
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Serine protease
 inhibitor

<400> 33
 Cys Lys Glu Tyr Glu Lys Gln Val Arg Asn Gly Arg Leu Phe Cys Thr
 1 5 10 15
 Arg Glu Ser Asp Pro Val Arg Gly Pro Asp Gly Arg Met His Gly Asn
 20 25 30
 Lys Cys Ala Leu Cys
 35

<210> 34
 <211> 37
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Serine protease
 inhibitor

<400> 34
 Cys Ser Gln Tyr Gln Asn Gln Ala Lys Asn Gly Ile Leu Phe Cys Thr
 1 5 10 15
 Arg Glu Asn Asp Pro Ile Arg Gly Pro Asp Gly Lys Met His Gly Asn
 20 25 30
 Leu Cys Ser Met Cys
 35

<210> 35
 <211> 37
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Serine protease
 inhibitor

<400> 35
 Cys Asn Glu Tyr Arg Lys Leu Val Arg Asn Gly Lys Leu Ala Cys Thr
 1 5 10 15
 Arg Glu Asn Asp Pro Ile Gln Gly Pro Asp Gly Lys Val His Gly Asn
 20 25 30
 Thr Cys Ser Met Cys
 35

<210> 36
 <211> 37
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Serine protease
 inhibitor

<400> 36
 Cys Ser Glu Tyr Arg Lys Ser Arg Lys Asn Gly Arg Leu Phe Cys Thr
 1 5 10 15
 Arg Glu Asn Asp Pro Ile Gln Gly Pro Asp Gly Lys Met His Gly Asn
 20 25 30

Thr Cys Ser Met Cys
35

<210> 37
<211> 37
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Serine protease
inhibitor

<400> 37
Cys Ser Glu Phe Arg Asp Gln Val Arg Asn Gly Thr Leu Ile Cys Thr
1 5 10 15

Arg Glu His Asn Pro Val Arg Gly Pro Asp Gly Lys Met His Gly Asn
20 25 30

Lys Cys Ala Met Cys
35

<210> 38
<211> 37
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Serine protease
inhibitor

<400> 38
Cys Ser Glu Tyr Arg His Tyr Val Arg Asn Gly Arg Leu Pro Cys Thr
1 5 10 15

Arg Glu Asn Asp Pro Ile Glu Gly Leu Asp Gly Lys Ile His Gly Asn
20 25 30

Thr Cys Ser Met Cys
35

<210> 39
<211> 37
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Serine protease
inhibitor

<400> 39
Cys Asp Glu Phe Arg Arg Leu Leu Gln Asn Gly Lys Leu Phe Cys Thr
1 5 10 15

Arg Glu Asn Asp Pro Val Arg Gly Pro Asp Gly Lys Thr His Gly Asn
 20 25 30

Lys Cys Ala Met Cys
 35

<210> 40

<211> 37

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Serine protease
 inhibitor

<400> 40

Cys Ala Glu Tyr Arg Glu Gln Met Lys Asn Gly Arg Leu Ser Cys Thr
 1 5 10 15

Arg Glu Ser Asp Pro Val Arg Asp Ala Asp Gly Lys Ser Tyr Asn Asn
 20 25 30

Gln Cys Thr Met Cys
 35

<210> 41

<211> 37

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Serine protease
 inhibitor

<400> 41

Cys Asp Glu Phe Arg Ser Gln Met Lys Asn Gly Lys Leu Ile Cys Thr
 1 5 10 15

Arg Glu Ser Asp Pro Val Arg Gly Pro Asp Gly Lys Thr His Gly Asn
 20 25 30

Lys Cys Thr Met Cys
 35